UNITED STATES PATENT AND TRADEMARK OFFICE **CERTIFICATE OF CORRECTION**

PATENT NO. : 7,402,660 B2

660 B2 Page 1 of 11

APPLICATION NO.: 09/918715
DATED: July 22, 2008
INVENTOR(S): Brad St. Croix et al.

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Prior to the Specification in Column 1, Line 1
Please insert the appended Tables 1-4.

Table 1. Previously characterized and novel Pan Endothelial Markers (PEMs).

The most abundant tags derived by summing the tags from Normal EC (N-EC's) and Tumor EC (T-EC's) SAGE libraries are listed in descending order. N-EC and T-EC SAGE libraries contained 96,694 and 96,588 SAGE tags respectively. For comparison, the corresponding number of SAGE tags found in cultured human umbilical vein endothelial cells (HUVEC), human dermal microvascular endothelial cells (HMVEC), and non-endothelial cell lines (Cell Lines) are shown. The HUVEC SAGE library contained 290,000 tags and the HMVEC library 111,000 tags. Non-endothelial cell lines consisted of 1.8x106 tags derived from a total of 14 different cancer cell lines including colon, breast, lung, and pancreatic cancers, as well as one non-transformed keratinocyte cell line, two kidney epithelial cell lines, and normal monocytes. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. The sequence CATG precedes all tags and the 15th base (11th shown) was determined as previously described by Velculescu et al. (Nat Genet 1999 Dec;23(4):387-8).

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Ceff Lines	Description
1	CATATCATTAA	ATCATTAA 247 S	501	130	87	2	angiomodulin (ANG, IGFBP-7, IGFBP-rP1, Mac25, TAF)
2	TGCACTTCAAG	328	141	0	0	0	hevin
3	TTTGCACCTTT	165	84	191	115	4	connective tissue growth factor (CTGF, IGFBP-rP2)
4	CCCTTGTCCG	131	104	1	1	0	ESTs
5	TTGCTGACTTT	73	131	2	14	1	collagen, type VI, alpha 1
6	ACCATTGGATT	102	67	0	0	2	Interferon induced transmembrane protein 1 (9-27, Leu 13)
7	ACACTTCTTTC	104	44	60	62	2	guanine nucleotide binding protein 11
8	TTCTGCTCTTG	71	67	118	72	0	von Willebrand factor
9	TCCCTGGCAGA	66	68	3	13	3	cysteine-rich protein 2 (CRP-2, ESP-1, SmLIM)
10	TAATCCTCAAG	26	106	34	16	1	collagen, type XVIII, alpha 1
11	ATGTCTTTTCT	58	65	17	17	3	insulin-like growth factor- binding protein 4
12	GGGATTAAAGC	40	67	30	14	2	CD146 (S-Endo 1, P1H12, Muc18, MCAM, Mel-CAM)
13	TTAGTGTCGTA	38	69	9	13	0	SPARC (osteonectin, BM-40)
14	TTCTCCCAAAT	20	86	16	64	2	collagen, type IV, alpha 2
15	GTGCTAAGCGG	24	74	0	10	2	collagen, type VI, alpha 2
16	GTTTATGGATA	35	56	11	11	1	matrix Gia protein (MGP)
17	CCCTTTCACAC	52	33	0	0	0	ESTs, Weakly similar to HPBRII-7 protein
	TGTTCTGGAGA	58	27	18	56	2	gap junction protein, alpha 1, 43kD (connexin 43)

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19	AAGATCAAGAT	34	50	2	4	1	actin, alpha 1, skeletal muscle / actin, alpha 2, smooth muscle, aorta
20	TCTCTGAGCAT	32	48	0	0	0	aggrecanase 1 (metalloproteinase with thrombospondin type 1 motifs, 4)
21	CAGGTTTCATA	22	56	0	0	0	small inducible cytokine subfamily B (Cys-X-Cys), member 14 (BRAK)
22	GCACAAGTTCT	43	25	6	22	0	calcitonin receptor-like receptor activity modifying protein 2
23	AGCTTGTGGCC	45	23	0	0	0	calcitonin receptor-like receptor activity modifying protein 3
24	CTTCTGGATAA	13	54	12	0	0	cell division cycle 42 (GTP- binding protein, 25kD)
25	CAACAATAATA	42	25	13	6	0	ESTs
26	ACCGGCGCCCG	50	15	0	0	0	tetranectin (plasminogen- binding protein)
27	GGAAGCTAAGT	35	27	0	5	1	osteoblast specific factor 2 (fasciclin I-like)
28	GCAATTTAACC	38	21	0	3	0	solute carrier family 21 (prostaglandin transporter), member 2
29	GATAACTACAT	18	35	4	4	0	anglomodulin (ANG, IGFBP-7, IGFBP-rP1, Mac25, TAF)
30	TATGAGGGTAA	19	30	40	2	0	regulator of G-protein signalling 5
31	CCACGGGATTC	10	39	0	0	0	collagen, type III, alpha 1
32	TTTACAAAGAG	26	21	0	1	1	carboxypeptidase E
33	CCCAGTAAGAT	22	25	0	16	1	cysteine and glycine-rich protein 2 (LIM domain only, smooth muscle)
34	ACAAAGCATTT	26	20	0	14	1	Human insulin-like growth factor binding protein 5 (IGFBP5) mRNA
35	GCCTGTCCCTC	8	38	22	11	0	ESTs / biglycan
36	TACTTTATAAG	25	21	1	1	0	metalloproteinase with thrombospondin type 1 motifs (ADAMTS1, METH-1)
37	TGTTTAATACA	15	29	2	1	1	ESTs / erythrocyte membrane protein band 4.1-like 2
38	GTCCCTGCCTT	18	25	1	1	0	glutathione S-transferase M2 (muscle)
39	GAGCCATCATA	21	21	2	2	1	ESTs / GTP-binding protein

	19 (M47901-0-4079) 2361-23 062(32)60-31-64 36-64 36-64 36-31-31		k editasteroviseus.	ĝi estan eras as antentarios capas s	14. gebenipus erpapi prapa pasienia	• 4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-	overexpressed in skeletal muscle		
40	GGCCCTACAGT	26	13	2	3	0	ESTs / KIAA0821 protein		
41	GCTAACCCCTG	7	31	0	1	0	ESTs		
42	ATCACACAGCT	19	18	0	0	0	thyroid and eye muscle autoantigen D1 (64kD)		
43	ACAAGTACTGT	18	19	36	27	0	cadherin 5, VE-cadherin (vascular epithelium)		
44	TCACCGTGGAC	20	17	0	1	0	selectin P (granule membrane protein 140kD antigen CD62)		
45	ACATTCCAAGT	18	18	0	1	1	tissue inhibitor of metalloproteinase 3		
46	GAGCCTGGATA	6	29	0	0	0	chondroitin sulfate proteoglycan 4 (melanoma-associated)		
47	GGCACTCCTGT	22	13	19	12	0	ESTS		
48	TCACAGCCCCC	20	15	8	5	0	ESTs		
49	TGCCAGGTGCA	10	23	0	1	0	albumin		
50	TGGGAAACCTG	11	22	0	1	1	eukaryotic translation initiation factor 4 gamma 1		
51	TTTCATCCACT	20	13	0	2	0	ESTs, KIAA0362 protein		
52	AACAGGGGCCA	15	18	0	0	1	ESTs / interferon, alpha- inducible protein (clone IFI-6-16)		
53	ACTGAAAGAAG	6	26	0	0	1	complement component 1 s subcomponent		
5 4	ACCGTTCTGTA	8	24	10	6	0	transcription factor 4		
55	ATACTATAATT	25	6	2	0	0	ESTS		
56	TTTGTATAGAA	17	15	4	5	1	KIAA0393 protein		
5 7	GTAATGACAGA	20	11	1	1	1	stanniocalcin		
5 8	AATAGGGGAAA	13	19	4	1	0	ESTs, KIAA1075 protein		
59	GTGCTACTTCT	5	25	2	18	0	collagen, type IV, alpha 1		
50	CCGGCCCCTCC	6	24	0	0	1	peanut (Drosophila)-like 2		
51	TTGAATTTGTT	19	10	1	1	0	RNA-binding protein gene. with multiple splicing		
52	CGAGAGTGTGA	22	6	0	0	0	ESTs		
53	CCCTGTTCAGC	14	15	38	24	0	tyrosine kinase with IgG and EGF homology domains (Tie)		
5 4	CAGATGGAGGC	18	10	1	9	0	ESTs .		
55	AGGCTCCTGGC	8	20	0	0	0	ESTs		
56	TCTGCTTCTAG	20	8	40	15	0	ESTs		

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67	GGCTTAGGATG	18	9	10	14	0	ESTs		
68	GGTTGTTGCG G	6	21	0	0	1	ESTS		
69	ACAAGTACCCA	5	22	4	5	0	P311 protein		
70	CTTCTCTTGAG	18	9	1	4	1	basic transcription elemen binding protein 1		
71	GCTAATAATGT	10	17	0	2	0	KIAA1077 protein		
72	TGTGCTTTTT	10	15	1	4	0	KIAA0758 protein / proteir kinase, cAMP-dependent, catalytic, alpha		
73	CATCACGGATC	17	8	0	1	0	interleukin 1 receptor, typ		
74	GCAGCAGCAGC	6	18	0	2	0	T-box 2		
195 75	TGACTGTATTA	13	11	0	0	0	ESTs / amine oxidase, copper containing 3 (vascular adhesion protein 1)		
76	GAATGCTCTTG	6	18	0	11	0	gap junction protein, alph 4, 37kD (connexin 37)		
77	GTAGTTCTGGA	18	6	0	5	0	ESTs, cione 23698 mRNA		
78	тсссстстстс	6	17	0	0	0	periodontal ligament fibroblast protein		
79	GGGCAGTGGCT	5	18	12	5	0	ESTs, DKFZP586B0621 protein		
80	AAATATGTGTT	19	4	13	3	0	ESTS		
81	GTCATTTTCTA	11	11	ideiskideiskises 10	2	0	ESTs / transcription factor 8 (represses interleukin 2 expression)		
82	CTCTCCAAACC	14	8	0	0	0	complement component 1 inhibitor (angioedema, hereditary)		
83	TTAATGTGTAA	4	18	0	0	0	guanylate cyclase 1, soluble, beta 3		
84	TCAAGCAATCA	13	9	0	1	0	ESTs		
85	GAAGACACTTG	15	7	1	0	0	ESTs		
86	GGGTAGGGTGA	6	15	0	0	1	Integrin, alpha 7		
87	TGGAACAGTGA	10	10	10	5	0	ESTs		
88 88	GAGTGGCTACC	10	9	0	0	0	ESTS		
 89	GTCAGGGTCCC	13	7	0	9	0	decidual protein induced to progesterone		
90	GTCAGTCACTT	14	6	4	1	0	hairy (Drosophila)-homol		
91	AGCAGAGACAA	14	6		10	0	natriuretic peptide recepto A - guanylate cyclase A		
92	AGCGATGGAGA	9	10	0	0	0	ESTS		
	જેન્સ્ટર્મન કરિયાનો સાથે કર્યો કર્યો કર્યો કર્યો કર્યો કર્યા છે. જેન્સ સ્થાર કર્યો કર્યો કર્યો કર્યો કર્યો કર્ય			**************	مفادة دعده المعاشدة ومردة ومكاوري	e giceskakońcecianie	rae is pessis išpasis riesis		

Table 2. Previously characterized and novel Tumor Endothelial Markers (TEMs).

The top 46 tags with the highest tumor EC (T-EC's) to normal EC (N-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis. †: multiple tags for this gene are due to alternative polyadenylation sites.

no.	Tag Sequence	N-EC's	T-EC's	HUVEC	HMVEC	Cell Lines	Description
1	GGGGCTGCCCA	0	28	0	2	0	TEM1
2	GATCTCCGTGT	0	25	0	0	0	TEM2
3	CATTITIATCT	0	23	0	0	0	TEM3
4	CTTTCTTTGAG	0	22	6	20	1	regulated in glioma-like 7-1 (Dkk-3/ REIC)
5	TATTAACTCTC	0	21	1	3	1	TEM4
6	CAGGAGACCCC	0	16	2	0	0	MMP-11 (stromelysin 3)
7	GGAAATGTCAA	1	31	53	22	1	MMP-2 (gelatinase A, 72kD type IV collagenease)
8	CCTGGTTCAGT	0	15	0	0	0	ESTs
9	TTTTTAAGAAC	0	14	1	4	0	TEM5
10	ттесттсс	5	139	0	16	0	collagen, type 1, alpha 2, transcript A
11	ATTTTGTATGA	0	13	4	8	0	nidogen (entactin)
12	ACTITAGATGG	1	23	0	15	0	collagen, type VI, alpha 3
13	GAGTGAGACCC	3	63	0	0	1	Thy-1 cell surface antigen
14	GTACACACACC	0	10	0	0	0	ESTs / cystatin S
15	CCACAGGGGAT	2	38	0	2	1	collagen, type III, alpha 1
16	TTAAAAGTCAC	1	19	1	3	1	TEM6
17	ACAGACTGTTA	4	74	0	0	0	TEM7
18	CCACTGCAACC	1	18	0	1	0	
19	CTATAGGAGAC	1	18	1	1	0	TEM8
20	GTTCCACAGAA	0	9	0	3	0	collagen, type I, alpha 2, transcript B
21	TACCACCTCCC	0	9	4	1	1	ESTs / pregnancy specific beta-1-glycoprotein 1
22	GCCCTTTCTCT	1	17	3	1	2	TEM9 (endo180 lectin)
23	TTAAATAGCAC	2	33	0	4	0	collagen, type I, alpha 1
24	AGACATACTGA	1	16	1	0	0	ESTs, DKFZP434G162 protein
25	TCCCCCAGGAG	1	16	0	0	0	bone morphogenetic protein 1 (metalloprotease)

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26	AGCCCAAAGTG	0	8	0	0	0	
27	ACTACCATAAC	0	8	0	0	0	slit (Drosophila) homolog 3 (MEGF5)
28	TACAAATCGTT	0	8	0	0	0	KIAA0672 gene product
29	TTGGGTGAAAA	0	8	0	0	0	ESTs
30	CATTATCCAAA	0	8	0	0	0	integrin, alpha 1
31	AGAAACCACGG	0	8	2	7	0	collagen, type IV, alpha 1
32	ACCAAAACCAC	0	8	0	3	0	page discontinue (do to
33	TGAAATAAAC	0	8	3	1	1	hate fastering bet a consequence of the established consequence of the
34	TTTGGTTTCC	1	15	0	0	0	ESTS
35	GTGGAGACGGA	1	15	1	2	1	ESTs
36	TTTGTGTTGTA	1	14	2	0	0	collagen, typeXII, alpha 1
37	TTATGTTTAAT	3	39	0	0	1	lumican
38	TGGAAATGACC	15	179	0	40	0	ESTs / collagen, type I, alpha 1
39	TGCCACACAGT	1	13	0	2	0	transforming growth factor, beta 3
40	GATGAGGAGAC	3	35	0	18	1	collagen, type I, aipha 2, transcript C1
41	ATCAAAGGTTT	2	23	0	0	0	ESTs, DKFZp5640222 mRNA
42	AGTCACATAGT	1	11	2	0	0	ESTs / cell division cycle 42 (GTP-binding protein)
43	ттсесттестс	4	45	0	19	0	त्राच्या ५ त्याच्या १८ तम् १९४४ १ १५ त्या देशके देशके दशके दश्य ग्राह्म १९ त्याच्या १८ तम् व्याप्त १८ व्याप्त १ इ.स.च. १९८८ १६ तम् १९४४ १ १५ त्याच्या १९४४ १ १ १ १ १ १ १ १ १ १ १ १ १ १ १ १ १
44	CCCCACACGGG	2	21	0	0	0	ESTs
45	GGCTTGCCTTT	1	10	0	10	1	racinalaladistribusum dubus alabek dishinga haladistrib
46	ATCCCTTCCCG	1	10	1	0	0	peanut-like protein 1

Table 3. Previously characterized and novel Normal Endothelial Markers (NEMs).

The top 33 tags with the highest normal EC (N-EC's) to tumor EC (T-EC's) tag ratios are listed in descending order. To calculate tag ratios, a value of 0.5 was assigned in cases where zero tags were observed. The SAGE libraries are the same as those listed in Table 1. Tag numbers for each group were normalized to 100,000 transcripts. A 'Description' of the gene product corresponding to each tag is given, followed by alternative names in parenthesis.

no.	o. Tag Sequence N		T-EC's	HUVEC	HMVEC	Cell Lines	Description	
1 TCTCACGTCTC		26	0	0	0	0	mucosal vascular addressin cell adhesion molecule 1	
2	CTAGCGTTTTA	19	0	4	14	0	serum deprivation response (phosphatidylserine-binding protein)	
3	GTGGCTGACGC	18	0	1	. 0	0	ESTs / Intercellular adhesion molecule 4	
4	CTCTTAAAAAA	34	1	1	0	0	small inducible cytokine subfamily A (Cys-Cys), member 14	
5	TGGGAAGAGGG	16	0	3	4	1	ESTs	
6	GTTTAAGGATG	16	0	0	0	0	ESTs	
7	сттетттес	15	0	56	32	1	endothelin 1	
8	ATTGCCAATCT	14	0	0	4	0	TU3A protein	
9	TGTTGAAAAA	21	1	1	0	0	E-selectin (endothelial adhesion molecule 1)	
10	ACAAAAAGGCC	21	1	0	6	0	TU3A protein	
11	AAGATGCACAC	21	1	1	1	1	phosphodiesterase I - nucleotide pyrophosphatase 2 (autotaxin)	
12	GTAGAGGAAAA	10	0	0	9	0	es - jus jus 1920 es 200 es 1910 em 1910 un 1910 es 1910 en 19 	
13	TTGTTCAAGGG	10	0	0	1	0	ESTs	
14	CTCTTCAAAAA	19	1	1	. 0	0	small inducible cytokine subfamily A, member 14	
15	TATTAAAATAG	18	1	6	9	1	transforming growth factor, beta receptor II (70-80kD)	
16	GAATTCACCAG	9	0	1	14	0	ESTs	
17	AAGGAGAACTG	9	0	0	0	0	small inducible cytokine subfamily A, member 14	
18	AATATCTGACT	9	0	2	2	2	active BCR-related gene	
19	TCAGTGACCAG	17	1	4		2	protein kinase C eta	
20	GCAAAGTGCCC	32	2	1	5	0	ESTs	
21	TAAATACTTGT	8	0			0	ESTs	

22	GTCACTAATTT	8	0	1	0	0	ESTs
23	ATAACCTGCAG	8	0	0	0	0	signaling lymphocytic activation molecule
24	TGCATCTGTGC	46	3	1	1	0	ESTs / glycogenin 2
25	TAAAGGCACAG	15	1	4	3	0	LIM binding domain 2
26	GACCGCGGCTT	73	5 .	11	7	0	claudin 5
27	ACTCCGGTGTG	14	1	0	8	0	ESTs
28	CTTCTCACCTA	27	2	3	1	0	GTP-binding protein
29	TCGTGCTTTGT	13	1	0	0	0	ESTs
30	GAGCAGTGCTG	13	1	4	2	1	feline sarcoma viral (v-fes) - Fujinami avian sarcoma viral (v-fps) homolog
31	СТСТАААААА	10	1	0	1	0	ESTs
32	GAAACCCGGTA	10	1	0	0	1	phospholipase C, beta 4
33	AACACAGTGCC	10	1	7	15	1	ESTs

Table 4. Detection of transcripts in various tumor types by RT-PCR and in situ hybridization (ISH).

The "+" sign indicates the presence of a robust RT-PCR product or stong positive staining of vessels by in situ hybridization. The "-" sign indicates an undetectable signal by in situ hybridization or an absent or barely detectable transcript by RT-PCR. The "+/-" sign indicates a very weak signal in a limited number vessels by in situ hybridization. "ND" indicates not determined.

		TEM1	TEM3	ТЕМ4	TEM5	TEM7	TEM8	TEM9	vWF	Hevin
RT-	ColonNor.	***************************************	-		1341.414.44		-		+	ND
PCR	Colon Tum.	+	+	+	+	+	+	+	+	ND
goden a maga	ColonNor.			•	•		•	-	+	+
	Colon Tum.	+	+	+	+	+	+	+	+	+
	Liver Met.	+	+/-	+	+	+	+	+	+/-	ND
ISH	Lung Tum.	-	ND	+	+	+	+	+	+	+
	Brain Tum.	+	ND	ND	ND	+	ND	ND	+	+*
	Corpus Lut.	+	+	+	+	+	•	+	+	+
	Wound	+	ND	+	ND	+/-	+/-	ND	+	+

^{*} hevin was localized to both endothelial cells and malignant cells in brain tissue.

UNITED STATES PATENT AND TRADEMARK OFFICE CERTIFICATE OF CORRECTION

PATENT NO. : 7,402,660 B2

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APPLICATION NO.: 09/918715
DATED: July 22, 2008
INVENTOR(S): Brad St. Croix et al.

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

In Column 40, Line 48

Please insert the following claims:

--33. The isolated molecule of claim 1 wherein said molecule binds to TEM17 at least 7 times more than to irrelevant antigen or antigen mixture.

34. The isolated molecule of claim 1 wherein said molecule binds to TEM17 at least 10 times more than to irrelevant antigen or antigen mixture.--

Signed and Sealed this

Twenty-eighth Day of October, 2008

JON W. DUDAS
Director of the United States Patent and Trademark Office